

GenCore version 5.1.4\_p5.4578  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: April 5, 2003, 04:01:18 ; Search time 122 Seconds  
(without alignments)

3163.556 Million cell updates/sec

Title: US-09-847-081B-2

Perfect score: 2270

Sequence: 1 MMSVALLWVSTSEVSG.....IYAKSLVPPNRTSPLAKT 440

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186958

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 10%

Listing first 45 summaries

Command line parameters:

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Database :

Published Applications\_NA:

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14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2270	100.0	1728	10	US-09-847-081B-1
2	1801	79.3	1712	10	US-09-847-081B-3
3	1737	76.5	1239	10	US-09-371-307-75
4	1542	67.9	1269	9	US-09-938-842A-729

5	350.5	15.4	1232	12	US-10-041-472-1	Sequence 1, Appli
6	336.5	14.8	891	9	US-09-941-947A-33	Sequence 33, Appl
7	326	14.4	8625	9	US-09-920-923-1	Sequence 1, Appli
8	326	14.4	11233	9	US-09-920-923-27	Sequence 27, Appl
9	324	14.3	908	10	US-09-547-267-4	Sequence 4, Appli
10	306	13.5	1020	9	US-09-918-740-71	Sequence 71, Appl
11	306	13.5	7252	9	US-09-918-740-73	Sequence 73, Appl
12	306	13.5	7252	9	US-09-918-740-75	Sequence 75, Appl
13	293	12.9	536165	9	US-09-939-964-1	Sequence 1, Appli
14	273.5	12.0	2174	7	US-08-781-986A-202	Sequence 202, App
15	204	9.0	912	9	US-09-738-626-695	Sequence 695, App
16	202.5	8.9	3309400	9	US-09-738-626-1	Sequence 1, Appli
17	198	8.7	876	9	US-09-738-626-2673	Sequence 2673, Ap
18	113	5.0	1242	9	US-09-938-842A-50	Sequence 50, Appl
19	112.5	5.0	114	9	US-10-103-450-12	Sequence 12, Appl
20	112.5	5.0	114	9	US-10-137-765-9	Sequence 9, Appli
21	112.5	5.0	114	9	US-10-146-337-9	Sequence 9, Appli
22	111.5	4.9	1606	10	US-09-820-004-1	Sequence 1, Appli
23	109.5	4.8	1662	10	US-09-917-800A-1669	Sequence 1669, Ap
24	109	4.8	17581	9	US-10-091-504-2170	Sequence 2170, Ap
25	109	4.8	17581	10	US-09-764-869-2170	Sequence 2170, Ap
26	109	4.8	40090	10	US-09-820-004-3	Sequence 3, Appli
27	103.5	4.6	1168	10	US-09-770-445-56	Sequence 56, Appl
28	103.5	4.6	13856	7	US-08-781-986A-31	Sequence 31, Appl
29	103	4.5	6613	12	US-10-032-717-28	Sequence 28, Appl
30	101	4.4	514	9	US-09-940-244-287	Sequence 287, App
31	101	4.4	1023	9	US-10-033-297-78	Sequence 78, Appl
32	101	4.4	1023	9	US-09-940-244-289	Sequence 289, App
33	101	4.4	1115	9	US-09-940-244-289	Sequence 289, App
34	101	4.4	3309400	9	US-09-738-626-1	Sequence 1, Appli
35	100.5	4.4	533	10	US-09-998-598-2126	Sequence 2126, Ap
36	99	4.4	19695	10	US-09-826-191-3	Sequence 3, Appli
37	97.5	4.3	1050	9	US-09-738-626-530	Sequence 530, App
38	97	4.3	996	9	US-09-938-842A-1379	Sequence 1379, Ap
39	96.5	4.3	48908	9	US-10-114-170-137	Sequence 137, App
40	95.5	4.2	30365	10	US-09-825-414-1	Sequence 1, Appli
41	94.5	4.2	1518	9	US-10-116-821-13	Sequence 13, Appl
42	94	4.1	1536	10	US-09-912-020-99	Sequence 99, Appl
43	93	4.1	1512	10	US-09-815-242-6983	Sequence 6983, Ap
44	92.5	4.1	2887	10	US-09-925-297-242	Sequence 242, App
45	92	4.1	1929	10	US-09-826-660-24	Sequence 24, Appl

#### ALIGNMENTS

RESULT 1  
US-09-847-081B-1  
; Sequence 1, Application US/09847081B  
; Patent No. US20020128464A1  
; GENERAL INFORMATION:  
; APPLICANT: BAYER AG  
; TITLE OF INVENTION: DNA encoding the tobacco phytoene synthase  
; FILE REFERENCE: Le 34 326  
; CURRENT APPLICATION NUMBER: US/09/847.081B  
; CURRENT FILING DATE: 2001-05-02  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1728  
; TYPE: DNA  
; ORGANISM: Nicotiana tabacum  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (244)..(1566)  
US-09-847-081B-1

Alignment Scores:  
Pred. No.: 2.47e-272 Length: 1728  
Score: 2270.00 Matches: 440  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0



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Qy 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMet---ThrVal 101
Db 501 -----TCGTAAAGTCTGCTATGCTGCTACACGGCGGAGAAATGGCAGCATG 551
Qy 102 SerSerGluLysLysValTyrAspValValLeuLysGlnAlaLeuValLysArgGln 121
Db 552 ACATCAGACAGATGGTTATGATGTTTAAACAGCAGCTTAGTAGAGGCGAG 611
Qy 122 LeuArgSerThrAspAspLeuGluValTyrProAspLysValValProGlyAsnLeuGly 141
Db 612 TTGAGATCTGCTGATGATTTAGAGTGAAGCGGAGATCCCTCTCCCGGGAATTTGAGC 671
Qy 142 LeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThrPhe 161
Db 672 TTGTTGAGTGAAGCATATGATAGTGTAGTGAAGTATGTCAGAGTATGCCAAGACATTT 731
Qy 162 TyrLeuGlyThrLysLeuMetThrProGluArgArgAlaLeuTyrAlaLysThrVal 181
Db 732 TACTTHGGAACCATGTAATGACTCCAGAGAGAAGGGCTATTGGGCAATATATGTG 791
Qy 182 TrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGln 201
Db 792 TGGTCAGAGACAGATGACTTGTGATGCGCCCAACGATCACATATTACACCCAA 851
Qy 202 AlaLeuAspArgTrpGluThrArgLeuGluAspLysPheSerGlyArgProPheAspMet 221
Db 852 GCCTTAGATAGTGGAGACCGCTTGAAGATGTTTTCAGCGGCGGACCATTTGATATG 911
Qy 222 LeuAspAlaAlaLeuSerAspThrValSerArgPheProValAspLysGlnPropheArg 241
Db 912 CTCGATGCTGCTTGTCCGATACGTTTCCAGATTTCCAGTTGATATTTCAGCGGTTCA 971
Qy 242 AspMetIleGluGlyMetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGlu 261
Db 972 GATATGATGAGGAATCCGTATGACTTGAGGAGTCAAGATATAGAACTTTGATGAG 1031
Qy 262 LeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProValMet 281
Db 1032 CTTTACCTCTATTGTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1091
Qy 282 GlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaLeuAlaLeu 301
Db 1092 GGTATGACCTTGATTCAGAGCAACACAGAGCGGTATATATGAGCTTTGCTTTA 1151
Qy 302 GlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgGly 321
Db 1152 GGAATCGCAATCACTAACGACATACACTCAGAGATGTTGGAGAGATGCCAGAGAGA 1211
Qy 322 ArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspLysPhe 341
Db 1212 AGAGTCTACTTACCTCAAGATGAATTAGCAGCGGAGCTCTCTTCGAGGATGACATATT 1271
Qy 342 AlaGlyArgValThrAspLysTrpArgAsnPheMetLysLysGlnIleGlnArgAlaArg 361
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Qy 362 LysPheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTrpPro 381
Db 1332 AAGTTCTTCGATGAGCAGAGAGAGAGTTACACAACTGAGCTCAGTACGAGATGGCT 1391
Qy 382 ValLeuThrAlaLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyr 401
Db 1392 GTATGGGATCTTCTGCTGTGTACCGCCAAATACCTGCGAGAGATTTGAAGCCAAATGACTAC 1451
Qy 402 AsnAsnPheThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuProIle 421
Db 1452 AACACTTCACAAAGAGCTTATGTGAGCAACCAAGAACTAATTTCTTACCTATT 1511
Qy 422 AlaTyrAlaLysSerLeuValProProAsnArgThr-SerSerProLeuAlaLys 439
Db 1512 GCTTATGCAAAATCTTGTGCGCCCTACAGAACTTGTGTCACCTCTAGCTAAG 1566

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RESULT 3

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US-09-371-307-75
; Sequence 75, Application US/09371307A
; Patent No. US20020053095A1
; GENERAL INFORMATION:
; APPLICANT: Brown, Sherri M.
; APPLICANT: Heck, Gregory R.
; APPLICANT: Piller, Kenneth J.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Elich, Ted D.
; APPLICANT: Logusch, Eugene W.
; APPLICANT: Rao, Sudabathula
; APPLICANT: Ream, Joel E.
; APPLICANT: Logusch, Sherry J.
; TITLE OF INVENTION: Methods for controlling gibberellin levels
; FILE REFERENCE: MOBT:216
; CURRENT APPLICATION NUMBER: US/09/371,307A
; CURRENT FILING DATE: 1999-08-10
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 75
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-371-307-75

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Alignment Scores:
Pred. No.: 3,02e-206 Length: 1239
Score: 1737.00 Matches: 342
Percent Similarity: 86.37% Conservative: 32
Best Local Similarity: 78.98% Mismatches: 35
Query Match: 76.52% Indels: 24
DB: 10 Gaps: 3

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US-09-847-081B-2 (1-440) x US-09-371-307-75 (1-1239)

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Db 58 TTCATGGAATCNGTCCGGAGGGAACCCGTTTGTGATTCATCG-----AGC 105
Qy 43 AspArgAsnLeuMetTrpAsnGlyArgIleLysLysGlyGlyArgGlnArgTrpAsnPhe 62
Db 106 CATAGGAATTTGGTGTCCAATCAGAGAATCAATAGAGT-----144
Qy 63 GlySerLeuIleAlaAspProArgTyrSerCysLeuGlyGlySerArgThrGluLysGly 82
Db 145 -----GGTGAAGCAAACTAATAATGGA 168
Qy 83 SerThrPheSerValGlnSerSerLeuValAlaSerProAlaGlyGluMetThrValSer 102
Db 169 CGGAATTTTCTGTACGGTCTGCTATTTTGGCTACTCTGAGAACGGAGCATGACA 228
Qy 103 SerGluLysLysValTyrAspValValLeuLysGlnAlaLeuValLysArgGlnLeu 122
Db 229 TCGGAACAGATGCTGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 288
Qy 123 ArgSerThrAspAspLeuValLysProAspIleValValProGlyAsnLeuLeu 142
Db 289 AGATCTACCAATGAGTGTAGAGTGAAGCGGATATACCTATTCCTCGGGGAATTTGGGCTTG 348
Qy 143 LeuSerGluAlaTyrAspArgCysGlyGluValCysAlaGluTyrAlaLysThrPheTyr 162
Db 349 TTGAGTGTAGCATATGATAGGTGTGCTGAGTATGTGAGAGTATGCCAAGAGCTTTAAC 408
Qy 163 LeuGlyThrLysLeuMetThrProGluArgArgAlaIleTrpAlaIleTyrValTrp 182
Db 409 TTAGGAACATGCTAATGACTCCGAGAGAAGAGGCTATCTGGCAATATATGATGG 468
Qy 183 CysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAla 202

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Db 469 TGCAGAAACACAGATGAATGTTGATGGCCAAACATCATATATATACCCGGCAGCC 528  
QY 203 LeuaspArgTrpGluThrArgLeuGluaspIlePheSerGlyArgProPheAspMetLeu 222  
Db 529 CTAGATAGGTGGGAAATAGCTAGAGATGTTTCAATAGGGGGCCATTGTGACATGCTC 588  
QY 223 AspAlaLeuSerAspThrValSerArgPheProValaspIleGlnProPheArgAsp 242  
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QY 263 TyrLeuTrpCysTrpTyrValAlaGlyThrValGlyLeuMetSerValProValMetGly 282  
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QY 283 IleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGly 302  
Db 769 ATCCGCCCTGAATCAAGGCAACACAGAGCGTATATATGCTGCTTGGCTCGCTGGG 828  
QY 303 LeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluaspAlaArgGlyArg 322  
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QY 323 ValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAla 342  
Db 889 GTCTACTGCTCAAGATGAATAGCACAGCGAGTCTATCCGATGAAGATATATTGCT 948  
QY 343 GlyArgValThrAspLysTrpArgAsnPheMetLysLysGlnIleGlnArgAlaArgLys 362  
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Db 1009 TTCTTGTATGAGGAGAGATGGCGTGACAGAAATTGAGCTCAGCTAGTATATCCCTGTA 1068  
QY 383 LeuThrAlaLeuLeuLeuTyrArgLysIleLeuaspGluIleGluAlaAsnAspTyrAsn 402  
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QY 403 AsnPheThrArgAlaTyrValSerLysProLysLysLysLeuLeuThrLeuProIleAla 422  
Db 1129 AACTTCAAGAGAGCATATGTGACGAATCAAGAAAGTTGATTGCTACCTATTGCA 1188  
QY 423 TyrAlaLysSerLeuValProAsnArgThrSerSer 435  
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## RESULT 4

US-09-938-842A-729  
; Sequence 729, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kieps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; PRIOR FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 729  
; LENGTH: 1369

; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-729

Alignment Scores: 5.71e-182 Length: 1269  
Pred. No.: 1542.00 Matches: 318  
Score: 81.86% Conservativity: 43  
Percent Similarity: 72.11% Mismatches: 51  
Best Local Similarity: 72.11% Indels: 30  
Query Match: 9 Gaps: 8  
DB: 9

US-09-847-081B-2 (1-440) x US-09-938-842A-729 (1-1269)

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QY 19 AsnGlyThrGlyLeuLeuAspSerValArgGluGlyAsnArgValPheValSerSerArg 38  
Db 61 AACAAATTGTGGTGGTA-----AGGTTCTAGAAATCTTCTAGA 99  
QY 39 PheLeuAlaArgAspArgAsnLeuMetTrpAsnGlyArgIleLysLysGly-GlyArgG1 58  
Db 100 CTGTCTCTCTCTTGTCTAG-----AATCAGAGACTAAACAAAGGTAAGAAGAAG 147  
QY 58 nArgTrpAsnPheGlySerLeuIleAlaAspProArgTrpTyrSerCysLeuGlyGlySerAr 78  
Db 148 CAGATACCAACTTGGAGTCTTCTT-----TTGTAAAGGAACCGA 186  
QY 78 gThrGluLysGlySerThrPheSerValGlnSerSerLeuValAlaLaserProAlaGlyG1 98  
Db 187 AGTAGAAGAAAT-CGTGTT-----GTGCTTCAAGCTTAGTAGCAAGCTCTTCTGGAGA 239  
QY 98 uMetThrValSerSerGluLysLysValTyrAspValValLeuLysGlnAlaLeuVal 118  
Db 240 GATAGCTCTTTCATCTCAAGAGAGGTTTCAATGTTGTGTTGAACAAGCTGCTTGGT 299  
QY 118 LysArgGlnLeuArgSerThrAsp-----AspLeuGluValLys-----ProAspIleVa 135  
Db 300 GAACAAACAGCTAAGGCTTCTTCTTATGACCTTGTGTGAAGAAACACCAAGATGTTGT 359  
QY 135 lValProGlyAsnLeuGlyLeuLeuSerGluAlaTyrAspArgCysGlyGluValCysAl 155  
Db 360 TCTTCTCGGGAGTTGAGTTGTTGGTGAAGCTTATGATCGATGCGGTGAAGTTTGGCG 419  
QY 155 aGluTyrAlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArgAl 175  
Db 420 TGAATATGCTAAGACGTTTATCTTGGAACTTGTCTTATGACACCCGAAAGCGAAGGC 479  
QY 175 aileTrpAlaIleTyrValTrpCysArgArgThrAspGluLeuValaspGlyProAsnAl 195  
Db 480 GATTGGGCAATCTACCTTGTGTAGAGAACTGATGAACCTTGTGGATGGGCCAAATGC 539  
QY 195 aSerHisIleThrProGlnAlaLeuAspArgTrpGluThrArgLeuGluAspIlePheSe 215  
Db 540 TTCATATTAACCTCCCATGGCTTTAGATAGTAGGAAGCAAGGATAGAAAGATCTTTCCG 599  
QY 215 rGlyArgProPheAspMetLeuAspAlaAlaLeuSerAspThrValSerArgPheProVa 235  
Db 600 TGGTCTGCTTTCGATATGCTTGTGATGCTCTCGCTGATACAGTTGCTAGATACCCCGT 659  
QY 235 lAspIleGlnProPheArgAspMetIleGluGlyMetArgMetAspLeuTrpLysSerAr 255  
Db 660 CGATATTTCAGCCATTTCGAGACATGATCGAAGGAATGAGATGGACTTGAAGAAATCGAG 719  
QY 255 gTyrLysThrPheAspGluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLe 275  
Db 720 ATACCAAGACTTCGATGATCTATACCTTACTGTCTACTACGCTGCGAAGCCGCTGGATT 779  
QY 275 uMetSerValProValMetGlyIleAlaProGluSerLysAlaThrThrGluSerValTy 295  
Db 780 GATGAGGCTTCCGCTTATGGGAATCGATCTTAACTCGAAGAAACCAACCAAGGTTTGA 839

QY 295 rsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValG1 315  
DB 840 CAACGCTGCTTGGCCCTTGGTATAGCCAATCAGCTTACTACATCTACAGAGCGTAGG 899  
QY 315 YGLuAspAlaArgGlyArgValTyLeuProGlnAspGluLeuAlaGlnAlaGlyLe 335  
DB 900 CGAATGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 959  
QY 335 uSerAspGluAspIlePheAlaGlyArgValTyLeuThrAspLysTyLeuArgAsnMetLysLy 355  
DB 960 TTCAGATGAGACATATTCCGCGGAAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTA 1019  
QY 355 sGlnIleGlnArgAlaArgLysPheAspGluSerGluLysGlyValThrGluLeuAs 375  
DB 1020 GCAGCTTAAACGAGCAAGAAATTTCTCGACGAGCTGAGAAAGCGTCACCGAGCTCAG 1079  
QY 375 pSerAlaSerArgTppProValLeuThrAlaLeuLeuLeuTyArgLysIleLeuAspG1 395  
DB 1080 TGCCGCTAGCATGGCTGTATGGCTTATGCTATGTAAGAGGAAATACTGGACGA 1139  
QY 395 ulleGluAlaAsnAspTyRAsnAsnPheThrArgAlaTyValSerLysProLysLy 415  
DB 1140 GATTGAAGCGAATGATTACACAAATTTACTAAGAGAGCTTATGTTGGGAAAGTCAAGAA 1199  
QY 415 sleuLeuThrLeuProIleAlaTyAlaLysSerLeuValProProAsnArgThrSerSe 435  
DB 1200 AATTCAGCTTGGCATTGGCTTATGCTAATCAATCAGTACTA-----AAGACTTCAAG 1250  
QY 435 x 435  
DB 1251 T 1251

## RESULT 5

US-10-041-472-1  
; Sequence 1, Application US/10041472  
; Patent No. US20020092039A1  
; GENERAL INFORMATION:  
; APPLICANT: Shewmaker, Christine  
; TITLE OF INVENTION: METHODS FOR PRODUCING CAROTENOID COMPOUNDS AND SPECIALITY OILS IN  
; TITLE OF INVENTION: SEEDS  
; FILE REFERENCE: 16516.141  
; CURRENT APPLICATION NUMBER: US/10/041,472  
; PRIOR FILING DATE: 2002-01-10  
; PRIOR APPLICATION NUMBER: US 08/908758  
; PRIOR FILING DATE: 1997-08-08  
; PRIOR APPLICATION NUMBER: US 60/024145  
; PRIOR FILING DATE: 1996-09-08  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1232  
; TYPE: DNA  
; ORGANISM: Erwinia uredovora  
US-10-041-472-1

## Alignment Scores:

Pred. No.: 9,4e-34 Length: 1232  
Score: 350.50 Matches: 110  
Percent Similarity: 43.88% Conservative: 55  
Best Local Similarity: 29.26% Mismatches: 162  
Query Match: 15.44% Indels: 49  
DB: 12 Gaps: 11

US-09-847-081B-2 (1-440) x US-10-041-472-1 (1-1232)

QY 77 SerArgThrGluLysGlySerThrPheSerValGlnSerSerLeuValAlaSerProAla 96  
DB 83 AGCCGCTGCTCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 127  
QY 97 Gly-----GluMetThrValSerSerGluLysLysValTyAspValValLeuLysGln 114  
DB 128 GCCTCAATTCATGCTGAGTCCAGTGAAGAGGTC----- 166

QY 115 AlaAlaLeuValLysArgGlnLeuArgSerThrAspLeuGluValLysProAsp--- 133  
DB 167 -----AACACTGACATTACTTCCATTACAGCAATGGT 199  
QY 134 -----IleValValProGlyAsnLeuGlyLeuLeuSerGluAlaTyArgCysGly 151  
DB 200 GGAAGAGTAAAGTGCATGAATATCCGCTGTTACTCAATCATCGCGTC----- 247  
QY 152 GluValCysAlaGluTyAlaLysThrPheTyLeuGlyThrLysLeuMetThrProGlu 171  
DB 248 GAACGATGGCGTAGTGGCTCGGAAAGTTTGGCAGCGCTCAAGATTATTGTGATGACAA 307  
QY 172 ArgArgArgAlaIleTyValTyAlaIleTyValTyCysArgArgThrAspGluLeuValAsp 191  
DB 308 ACCCGCGCAGCGTACTGATGCTCTACGCTGGTGGCGCATTTGTCAGCATGTTATTGAC 367  
QY 192 GlyProAsn-----AlaSerHisIleThrProGlnAlaLeu 203  
DB 368 GATCAGACGCTGGGCTTTTCAGGCGCGGCGAGCTGCTTACAAACGCCCGCAACGCTCTG 427  
QY 204 AspArgTtpGluThrArgLeuGluAspIlePheSerGly---ArgProPheAspMetLeu 222  
DB 428 ATGCAACTTGAGATGAAGAACGCCGAGCGCTATGCGAGGATGCGAGATGCGAACCGGCG 487  
QY 223 AspAlaAlaLeuSerAspThrValSerArgPheProValAspIleGlnProPheArg--- 241  
DB 488 TTTGCGGCTTTTCAGGAAGTGGCTATGGCTCAT-----GATATCCCGCGGCTTACGCG 541  
QY 242 ---AspMetIleGluGlyMetArgMetAspLeuTyLysSerArgTyLysThrPheAsp 260  
DB 542 TTTGATCATCTGGAAGGCTTCGCCATGGATGTACGCGAAGCGCAATACAGCAACTGGAT 601  
QY 261 GluLeuTyLeuTyCysTyTyValAlaGlyThrValGlyLeuMetSerValProVal 280  
DB 602 GATACGCTGGCTATTGCTATCAGCTTGCAGCGCTTGTGCGGTGTGATGATGGCGCAAT 661  
QY 281 MetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyRAsnAlaAlaLeuAla 300  
DB 662 ATGGGCGTG-----CGGGATAACGCCCGCTGGAC-----CGCGCCTCTGAC 703  
QY 301 LeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArg 320  
DB 704 CTGGGCTGGCATTTTCAGTTGACCAATATTGCTCGCGATATTGTGACGATGCGCATGCG 763  
QY 321 GlyArgValTyLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIle 340  
DB 764 GGCCGCTGTTATCTCGCGCAAGCTGGCTGGAGCATGAAGGCTGAACAAAGAGATTAT 823  
QY 341 PheAlaGlyArgValThrAspLysTyRAsnPheMetLysLysGlnIleGlnArgAla 360  
DB 824 GCGGCACCTGAAAACCGTCAGCGCTGAGCCGCTATCGCCGCTGTTGTTGTCAGGAAGCA 883  
QY 361 ArgLysPhePheAspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTrp 380  
DB 884 GAACCTTACTATTGCTGTCACAGCGCGCTGGCAGGCTTGCCTCGCTTCCGCTGG 943  
QY 381 ProValLeuThrAlaLeuLeuLeuTyArgLysIleLeuAspGluIleGluAlaAsnAsp 400  
DB 944 GCAATCGCTACGGCGAAGCAGGAGGTTTACCGGAAATAGGTGTCAAGATTGAACAGCGCG 1003  
QY 401 TyRAsnAsnPheThrArgArgAlaTyValSerLysProLysLysLeuLeuThrLeuPro 420  
DB 1004 CAGCAAGCCTGGGATCAGCGGAGTCAACGACCGCCCGCGGAAATTAACGCTGCTGCTG 1063  
QY 421 IleAlaTyAlaLysSerLeuValProProAsnArgThrSerSerPro 436  
DB 1064 GCGCGCTCTGTCAGCGGCTTACTCCCGGATGCGGCTCATCTCTCCC 1111

## RESULT 6

US-09-941-947A-33  
; Sequence 33, Application US/09941947A  
; Publication No. US20030003528A1

```

; GENERAL INFORMATION:
; APPLICANT: Brzostowicz, Patricia C.
; APPLICANT: Cheng, Qiong
; APPLICANT: DiCosimo, Deana J.
; APPLICANT: Koffas, Mattheos
; APPLICANT: Miller, Edward S. Jr.
; APPLICANT: Odum, J. Martin
; APPLICANT: Picastaglio, Steve
; APPLICANT: Rouvere, Pierre E.
; TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
; FILE REFERENCE: CL1903 US NA
; CURRENT APPLICATION NUMBER: US/09/941-947A
; PRIOR APPLICATION NUMBER: 60/229,907
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: 60/229,858
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 33
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Pantoea stewartii
; US-09-941-947A-33

Alignment Scores:
Pred. No.: 3,15e-32 Length: 891
Score: 336.50 Matches: 88
Percent Similarity: 48.28% Conservative: 52
Best Local Similarity: 30.34% Mismatches: 131
Query Match: 14.8% Indels: 19
DB: 6 Gaps: 6

US-09-847-081B-2 (1-440) x US-09-941-947A-33 (1-891)
QY 158 AlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTTP 177
DB 13 TCGAAAGTTCGCGACTGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 72
QY 178 AlaIleTyrValTrpCysArgArgThrAspGluLeuValAspGlyProAsn----- 194
DB 73 ATGCTTACGCATGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 132
QY 195 -----AlaSerHisIleThrProGluAlaLeuAspArgTrpGluThrArg 209
DB 133 CATGCGCGACCGCTCTTCGCGAGATGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 192
QY 210 LeuGluAspIlePheSerGly---ArgProPheAspMetLeuAspAlaLeuSerAsp 228
DB 193 ACAGCTCAGCGCTACCGCGGTCGCAATGACGCGCGCGCGCGCGCGCGCGCGCGCG 252
QY 229 ThrValSerArgPheProValAspIleGlnProPheArg-----AspMetIleGluGly 246
DB 253 GTGCGCGATGCGCGAT-----GATATCGCTCGCGCGCGCGCGCGCGCGCGCGCG 306
QY 247 MetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspClnLeuTyrLeuTyrCys 266
DB 307 TTGCGCATGATGCGCGAAGCGCGCTACCTGACACTGCGCGCGCGCGCGCGCGCGCG 366
QY 267 TyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGlyIleAlaProGlu 286
DB 367 TATCAGCTCGCGCGTCTTGGCGCGCTGATGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 287 SerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGln 306
DB 421 GATAAGCGCACGCTCAT-----CGCGCGCTGCGATCTCGCGCGCGCGCGCGCG 468
QY 307 LeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGlyArgValTyrLeuPro 326
DB 469 TTGACCAACATTCGCGGTGATATGCGGAGATGCTCAGGCGCGCGCGCGCGCGCG 528
QY 327 GlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaGlyArgValThr 346
DB 4286 -----GCCATCGCGCGAGGTTTCGCAAGGCTTCGCGCGCGCGCGCGCGCG 4233

GENERAL INFORMATION:
; APPLICANT: Brzostowicz, Patricia C.
; APPLICANT: Cheng, Qiong
; APPLICANT: DiCosimo, Deana J.
; APPLICANT: Koffas, Mattheos
; APPLICANT: Miller, Edward S. Jr.
; APPLICANT: Odum, J. Martin
; APPLICANT: Picastaglio, Steve
; APPLICANT: Rouvere, Pierre E.
; TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
; FILE REFERENCE: CL1903 US NA
; CURRENT APPLICATION NUMBER: US/09/941-947A
; PRIOR APPLICATION NUMBER: 60/229,907
; PRIOR FILING DATE: 2001-09-01
; PRIOR APPLICATION NUMBER: 60/229,858
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 33
; LENGTH: 891
; TYPE: DNA
; ORGANISM: Pantoea stewartii
; US-09-941-947A-33

Alignment Scores:
Pred. No.: 3,15e-32 Length: 891
Score: 336.50 Matches: 88
Percent Similarity: 48.28% Conservative: 52
Best Local Similarity: 30.34% Mismatches: 131
Query Match: 14.8% Indels: 19
DB: 6 Gaps: 6

US-09-847-081B-2 (1-440) x US-09-941-947A-33 (1-891)
QY 158 AlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleTTP 177
DB 13 TCGAAAGTTCGCGACTGCGCGCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 72
QY 178 AlaIleTyrValTrpCysArgArgThrAspGluLeuValAspGlyProAsn----- 194
DB 73 ATGCTTACGCATGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 132
QY 195 -----AlaSerHisIleThrProGluAlaLeuAspArgTrpGluThrArg 209
DB 133 CATGCGCGACCGCTCTTCGCGAGATGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 192
QY 210 LeuGluAspIlePheSerGly---ArgProPheAspMetLeuAspAlaLeuSerAsp 228
DB 193 ACAGCTCAGCGCTACCGCGGTCGCAATGACGCGCGCGCGCGCGCGCGCGCGCGCG 252
QY 229 ThrValSerArgPheProValAspIleGlnProPheArg-----AspMetIleGluGly 246
DB 253 GTGCGCGATGCGCGAT-----GATATCGCTCGCGCGCGCGCGCGCGCGCGCGCG 306
QY 247 MetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspClnLeuTyrLeuTyrCys 266
DB 307 TTGCGCATGATGCGCGAAGCGCGCTACCTGACACTGCGCGCGCGCGCGCGCGCGCG 366
QY 267 TyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGlyIleAlaProGlu 286
DB 367 TATCAGCTCGCGCGTCTTGGCGCGCTGATGCGCGCGCGCGCGCGCGCGCGCGCG 420
QY 287 SerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsnGln 306
DB 421 GATAAGCGCACGCTCAT-----CGCGCGCTGCGATCTCGCGCGCGCGCGCGCG 468
QY 307 LeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGlyArgValTyrLeuPro 326
DB 469 TTGACCAACATTCGCGGTGATATGCGGAGATGCTCAGGCGCGCGCGCGCGCGCG 528
QY 327 GlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaGlyArgValThr 346
DB 4286 -----GCCATCGCGCGAGGTTTCGCAAGGCTTCGCGCGCGCGCGCGCGCG 4233

```



QY 396 IleGluAlaAsnAspTyrAsnAsnPhetThrArgArgAlaTyrValSerLysProLysLys 415  
 Db 4245 ATCCGCGAGGTGGCCCGGAGGCTATCCGACGCGGATCAGCAGCTCGAAGGCTGCCAAG 4186  
 QY 416 Leu 416  
 Db 4185 ATC 4183

## RESULT 9

US-09-547-267-4  
 ; Sequence 4, Application US/09547267  
 ; Patent No. US20020147371A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hohmann, Hans-Peter  
 ; APPLICANT: Pasamontes, Luis  
 ; APPLICANT: Tessier, Michel  
 ; APPLICANT: van Loon, Adolphus  
 ; TITLE OF INVENTION: FERMENTATIVE CAROTENOID PRODUCTION  
 ; NUMBER OF SEQUENCES: 47  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Hoffmann-La Roche Inc.  
 ; STREET: 340 Kingsland Street  
 ; CITY: Nutley  
 ; STATE: NJ  
 ; COUNTRY: USA  
 ; ZIP: 07110  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/547,267  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/660,645  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Pokras, Bruce A.  
 ; REGISTRATION NUMBER: 32,748  
 ; REFERENCE/DOCKET NUMBER: RAN 6002/170  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (201) 235-5801  
 ; TELEFAX: (201) 235-2363  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 908 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-09-547-267-4

Alignment Scores:  
 Pred. No.: 1,166-30 Length: 908  
 Score: 324.00 Matches: 95  
 Percent Similarity: 48.3% Conservatives: 39  
 Best Local Similarity: 34.30% Mismatches: 111  
 Query Match: 14.27% Indels: 32  
 DB: 10 Gaps: 10

US-09-847-081b-2 (1-440) x US-09-547-267-4 (1-908)

QY 155 AlaGluTyrAlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArg 174  
 Db 37 GCGCAGGTTTCGAAGCTTCGCGAGGCGGCAAGCTGATCCGCGCGCATCCGCGAG 96  
 QY 175 AlaIleTyrAlaLysThrPheTyrLeuGlyThrLysLeuMetThrProGluArgArg 192  
 Db 97 GATACGGTATCTCTATCCCTGCGAGGATCGGATGACGTGATCGACGCGGAGTG 156  
 QY 193 -----ProAsnAlaSerHisIleThrProGlnAla----- 202

Db 157 ATGGGTTCGCCCGAGCGCGCGGC-----GACCCACAGCGCGGTGGGGCGCTCGCG 213  
 QY 203 LeuAspArgTyrPheGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMetLeu 222  
 Db 214 GCGCACAGCTGCGCGCGTGCACGAGGACGCCGATTCGCCGCCCTTC----- 264  
 QY 223 AspAlaAlaLeuSerAspThrValSerArg-----PheProValAspIleGlnProPhe 240  
 Db 265 ---GCGGCGCTCGCCAGGTGCGCGCGCGCATGATTCCCG---CACCTTTGCGCGCATG 318  
 QY 241 ArgAspMetIleGluGlyMetArgMetAspLeuTyrPheSerArgTyrLysThrPheAsp 260  
 Db 319 ---GACCTGATCGAGGTTTCGCGATGATGCGCGGATCGCGAATACCGACCGCTGGAT 375  
 QY 261 GluLeuTyrLeuTyrCysTyrTyrValAlaGlyThrValGlyLeuMetSerValProVal 280  
 Db 376 GACGTGCTGGAATATCTACACGCTCGCGGGGCTGCGGCGTGATGATGCGCGCGGTG 435  
 QY 281 MetGlyIleAlaProGluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAla 300  
 Db 436 ATGGCGGTG-----CAGGACGATGCGGTGCTGCTGATCGCGCTCGCAT 477  
 QY 301 LeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArg 320  
 Db 478 CTGGGCGCTTGGCTTCAGCTGACGACATCGCTCGCGAGCTGATCGACATCGCGCATC 537  
 QY 321 GlyArgValTyrLeuProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIle 340  
 Db 538 GGGCGCTGCTATCTGCTGCCACTGCTGCGCGGAGCGGGCGGCGGTGAG----- 591  
 QY 341 PheAlaGlyArgVal---ThrAspLysTyrArgAsnPhetMetLysLysGlnIleGlnArg 359  
 Db 592 -----GGTCCGCTGCTTCGCGACGCGCTCTATTTCGTGTCATCATCGCGCTGTTGACGCG 645  
 QY 360 AlaArgLysPheAspGluSerGlyLysGlyValThrGluLeuAspSerAlaSerArg 379  
 Db 646 GCGGAGCGCTATATGCTCGCGGCGGAGGCGTTCGCGCATCTGCGCGCGCGCTCGCGG 705  
 QY 380 TrpProValLeuThrAlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsn 399  
 Db 706 TGGTCGATCGCGCGCGCTGCGTATCTATCGGCAATCGGACGCGCATCGCGCGAGGT 765  
 QY 400 AspTyrAsnAsnPhetThrArgArgAlaTyrValSerLysProLysLysLeu 416  
 Db 766 GCGCCCGAGGCGCTATCGCGACGCGGATCAGCAGCTCGAAGGCTGCCAAGATC 816

## RESULT 10

US-09-918-740-71  
 ; Sequence 71, Application US/09918740  
 ; Publication No. US20030033626A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hahn, Frederick  
 ; APPLICANT: Kuehnle, Adelheid  
 ; TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathway  
 ; FILE REFERENCE: KAS-103XCI  
 ; CURRENT APPLICATION NUMBER: US/09/918,740  
 ; CURRENT FILING DATE: 2001-07-31  
 ; PRIOR APPLICATION NUMBER: 60/221,703  
 ; PRIOR FILING DATE: 2000-07-31  
 ; NUMBER OF SEQ ID NOS: 76  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 71  
 ; LENGTH: 1020  
 ; TYPE: DNA  
 ; ORGANISM: Rhodobacter capsulatus  
 ; US-09-918-740-71

Alignment Scores:  
 Pred. No.: 2,416-28 Length: 1020  
 Score: 306.00 Matches: 90  
 Percent Similarity: 48.79% Conservatives: 51

Best Local Similarity: 31.14% Mismatches: 130  
 Query Match: 13.48% Indels: 18  
 DB: 9 Gaps: 6

US-09-847-081B-2 (1-440) x US-09-918-740-71 (1-1020)

```

Qy 152 GluValCysAlaGluTyrAlaLysThr-----PheTyrLeuGlyThrLysLeu 167
Db 22 GAGTCTCCGGGAGCTATCCGACCGGAGCTACTCTTCCATGCGGCGCTCCAGAGT 81
Qy 168 MetThrProGluArgArgAlaIleThrPalalIleTyrValTyrCysArgThrAsp 187
Db 82 CTGCGCGCGGGTCCCTGACCGCGCTGCTTACGCTTTTGGCGGTGCGCGAT 141
Qy 188 GluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArgTrpGlu 207
Db 142 GACGAAGTCGAGAGGTGGCGCGCGGACGAGGCTGCGGCGGTTTGAACACTGGC 201
Qy 208 ThrArgLeuGluAspIlePheSerGlyArgProPheAspMet---LeuAspAlaLeu 226
Db 202 GACGCGCTGGAGGACATCTATGCGGTGCTCCGCGCAATGCGCCCTCGGCTTTC 261
Qy 227 SerAspThrValSerArgPheProValAspIleGlnProPheArgAspMetIleGluGly 246
Db 262 CGCGCGGTGTCGAGGAATCGAGATCGCGCGCAATGCGCGAGGCTCTCGAGGCG 321
Qy 247 MetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGluLeuTyrLysCys 266
Db 322 TTCGCTGGATCGGAGGCGGTGTTATCACACGCTTTTCGAGCTGTCAGGCTATTCG 381
Qy 267 TyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGlyIleAla---Pro 285
Db 382 CGCGCGGTGGCGCGCGCTGCGCGCGATGATGCTGCTGATGCGGCGGCTTTCCTG 540
Qy 286 GluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsn 305
Db 442 GATGCGCTGGCG-----CGGCGCTCGATCTCGGTCTTGCCATG 480
Qy 306 GlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgGlyArgValTyrLeu 325
Db 481 CAGATGTGGAACATCGCCCGGAGCTGGCGGAGGATGCGCGGCGGCGGCTTTCCTG 540
Qy 326 ProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaGly---Arg 344
Db 541 CCGACCGACTGGATGCTGCGGAGGAGGATGATCCGAGGCGTTCCTGCGCGACCGCAG 600
Qy 345 ValThrAspLysTrpArgAsnPheMetLysLysGlnIleGlnArgAlaArgLysPhePhe 364
Db 601 CCCACGAGGATCCCGCGGCTACCGAGCGGTGCTGTAACCGCGCGGCGGCTTTCAT 660
Qy 365 AspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTrpProValLeuThr 384
Db 661 TGGCGGGGCGGAGCGGGGTGCGCTTTGCGCTTTCGCTGCGCGCGGAGTATGCGC 720
Qy 385 AlaLeuLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyrAsnAspPhe 404
Db 721 CGGCGCAAGATCTATGCGCGATCGGCGCGGAGGTGCGGAAGGCGGAATACGACAACATC 780
Qy 405 ThrArgArgAlaTyrValSerLysProLysLysLeuLeuThrLeuPro----- 420
Db 781 ACCGCGGTGCCACACGACCGAGGCGCGAAGCTGCGGTGGTGGGAATTCGCGCATG 840
Qy 421 IleAlaTyrAlaLysSerLeuValPro 429
Db 841 TCGCGAGCGGACCTCGATCGCG 867

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## RESULT 11

US-09-918-740-73  
 ; Sequence 73, Application US/09918740  
 ; Publication No. US20030033626A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hahn, Frederick  
 ; APPLICANT: Kuehnle, Adelheid

```

; TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid path
; TITLE OF INVENTION: create novel traits in transgenic organisms
; FILE REFERENCE: KAS-103XCI
; CURRENT APPLICATION NUMBER: US/09/918,740
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/221,703
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 73
; LENGTH: 7252
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..( )
; OTHER INFORMATION: Plastid transformation vector pHK07, containing Operon C, cc
; OTHER INFORMATION: 1
; US-09-918-740-73

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## Alignment Scores:

Pred. No.: 4,98e-27 Length: 7252  
 Score: 306.00 Matches: 90  
 Percent Similarity: 48.79% Conservative: 51  
 Best Local Similarity: 31.14% Mismatches: 130  
 Query Match: 13.48% Indels: 18  
 DB: 9 Gaps: 6

US-09-847-081B-2 (1-440) x US-09-918-740-73 (1-7252)

```

Qy 152 GluValCysAlaGluTyrAlaLysThr-----PheTyrLeuGlyThrLysLeu 167
Db 4143 GAGTCTCCGGGAGCTATCCGACCGGAGCTACTCTTCCATGCGGCGCTCCAGAGT 4202
Qy 168 MetThrProGluArgArgAlaIleThrPalalIleTyrValTyrCysArgThrAsp 187
Db 4203 CTGCGCGCGGGTCCCTGACCGCTGCGGCTTACGCTTTTGGCGGTGCGCGAT 4262
Qy 188 GluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArgTrpGlu 207
Db 4263 GACGAAGTCGAGGAGTGGCGCGCGGCGGCAAGGTCGCGGCTTTGAACTGGC 4322
Qy 208 ThrArgLeuGluAspIlePheSerGlyArgProPheAspMet---LeuAspAlaLeu 226
Db 4323 GACCGCTGGAGGACATCTATGCGGCTGCTGCGCGCAATGCGCCCTCGGCTTTC 4382
Qy 227 SerAspThrValSerArgPheProValAspIleGlnProPheArgAspMetIleGluGly 246
Db 4383 CGCGCGGTGGTTCGAGGAATTCGAGATGCGCGCGAATTCGCCGAGCGGCTGCTGGAGGC 4442
Qy 247 MetArgMetAspLeuTrpLysSerArgTyrLysThrPheAspGluLeuTyrLysCys 266
Db 4443 TTCGCTGGGATGCGGAGGCGGTGGTATCACAGCTTTTCGAGCTGCGAGGCTATTCG 4502
Qy 267 TyrTyrValAlaGlyThrValGlyLeuMetSerValProValMetGlyIleAla---Pro 285
Db 4503 CGCGCGGTGGCGCGCGCTGCGCGGATGATGCTGCTGCTGATGCGGCTGCGCAACCC 4562
Qy 286 GluSerLysAlaThrThrGluSerValTyrAsnAlaAlaLeuAlaLeuGlyLeuAlaAsn 305
Db 4563 GATCGCTGGCG-----CGGCGCTGCGATCTCGGTCTTGCCATG 4601
Qy 306 GlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgValTyrLeu 325
Db 4602 CAGATGTGGAACATCGCCCGGAGCTGGCGGAGGATGCGCGGCGGCGGCTTTTCCTG 4661
Qy 326 ProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaGly---Arg 344
Db 4662 CCGACCGACTGATGCTGCGAGGAGGATGATGATCCGAGGCGTTCCTGCGCGCTCCGAG 4721
Qy 345 ValThrAspLysTrpArgAsnPheMetLysLysGlnIleGlnArgAlaArgLysPhePhe 364
Db 4722 CCCACGAGGATCCCGCGGCTACCGCGGCTGCTGTAACCGCGCGGCGGCTTTCAT 4781

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QY 365 AspGluSerGluYsGlyValThrGluLeuAspSerAlaSerArgTrpProValLeuThr 384  
Db 4782 TGGCGGGCGGCGACGGGGTGGGCTTTTGGCTTGGCTGCGCGGGGATCGGCC 4841  
QY 385 AlaLeuLeuLeuYsArgGlyValThrGluLeuAspGluLeuGluAlaAsnAspTrpAsnAsnPhe 404  
Db 4842 GCGGGCAAGATCTATGCGCGATCGGGCGGAGTGGCGAAGCGGAATACACACATC 4901  
QY 405 ThrArgAlaValSerLysProLysLysLeuLeuThrLeuPro----- 420  
Db 4902 ACCGGCGTGGCCACACAGCAAGCGCGCAAGCTGTGGCTGGTGGCGAATTCGCGATG 4961  
QY 421 IleAlaValAlaLysSerLeuValPro 429  
Db 4962 TCGCGGACGGCGACCTCGATGTCGCG 4988

## RESULT 12

US-09-918-740-75  
; Sequence 75, Application US/09918740  
; Publication No. US20030033826A1  
; GENERAL INFORMATION:  
; APPLICANT: Hahn, Frederick  
; TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways  
; FILE REFERENCE: KAS-103XCI  
; CURRENT APPLICATION NUMBER: US/09/918,740  
; CURRENT FILING DATE: 2001-07-31  
; PRIOR APPLICATION NUMBER: 60/221,703  
; PRIOR FILING DATE: 2000-07-31  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 75  
; LENGTH: 7252  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)..()  
; OTHER INFORMATION: Plasmid transformation vector pPHO5 containing R. capsulatus DNA  
US-09-918-740-75.

## Alignment Scores:

Pred. No.:	4,98e-27	Length:	7252
Score:	306.00	Matches:	90
Percent Similarity:	48.79%	Conservative:	51
Best Local Similarity:	31.14%	Mismatches:	130
Query Match:	13.48%	Indels:	18
DB:	9	Gaps:	6

US-09-847-081B-2 (1-440) x US-09-918-740-75 (1-7252)

QY 152 GluValCysAlaGluValAlaLysThr-----PheYrLeuGlyThrLysLeu 167  
Db 4143 GAGGTCTGCGGGAGTGTCCGACCGGAGCTACTCTTCATCGCGGGTCCAGATT 4202  
QY 168 MetThrProGluArgArgAlaLysThrAlaLysValThrCysArgArgThrAsp 187  
Db 4203 CTGCGGCGGGTCTGCGTACCGCGCTGGCGCTTTTACGCTTTTGGCGGTCGCGAT 4262  
QY 188 GluLeuValAspGlyProAsnAlaSerHisIleThrProGlnAlaLeuAspArgTrpGlu 207  
Db 4263 GACGAAGTCGACGAGTGTGGCGCGCGCGACAAAGCTGCGCGGCTTTGAACTTGGC 4322  
QY 208 ThrArgLeuGluAspPheSerGlyArgProPheAspMet--LeuAspAlaLeu 226  
Db 4323 GACCGCTGGAGGACATCTATGCGGTCTGCGCGGCAATGCGGCCCTCGGATCGGGCTTC 4382  
QY 227 SerAspThrValSerArgPheProValAspIleGlnProPheArgAspMetIleGluGly 246  
Db 4383 GCGGCGGTGTCGAGGAATTCGAGATGCGCGCGGAATTCGCCGAGCGGCTGCTGGAGGCG 4442

QY 247 MetArgMetAspLeuTrpLysSerArgTrpLysThrPheAspGluLeuThrLysCys 266  
Db 4443 TTCGCTGCGGTGCGGAGGCGGGTGGTATCACACGCTTTCGACGCGAGGCGCTATCG 4502  
QY 267 TyrTrpValAlaGlyThrValGlyLeuMetSerValProValMetGlyIleAla---Pro 285  
Db 4503 GCGCGGGTGGCGGCGCGCTGCGCGGATGATGTGGCTGCTGATCGGTCGCGACACCC 4562  
QY 286 GluSerLysAlaThrThrGluSerValTyAsnAlaLeuAlaLeuGlyLeuAlaAsn 305  
Db 4563 GATGCGCTGGCG-----CGGGCCTGGCATCTCGGTCTTGCATG 4601  
QY 306 GlnLeuThrAsnIleLeuArgAspValGlyGluAspAlaArgArgGlyArgValLeu 325  
Db 4602 CAGATGTGCAACATCGCCCGCGACGCTGGCGAGGATGCCCGGCGGGCGGCTTTCTCTG 4661  
QY 326 ProGlnAspGluLeuAlaGlnAlaGlyLeuSerAspGluAspIlePheAlaGly---Arg 344  
Db 4662 CCGACCGACTGATGTCGAGGAGGATCGATCCCGAGCGTTCCTGGCGGATCGCGAG 4721  
QY 345 ValThrAspLysTrpArgAsnPheMetLysLysGlnIleGlnArgAlaArgLysPhePhe 364  
Db 4722 CCACCAAGGGCATCGCGGGTCCACCGAGGCTTGTGAACCGCGCGCGCTTAC 4781  
QY 365 AspGluSerGluYsGlyValThrGluLeuAspSerAlaSerArgTrpProValLeuThr 384  
Db 4782 TGGCGGGCGGCGACGGGGTGGGCTTTTGGCTTTGCTGCTGCGGCGCGGATCGGCGC 4841  
QY 385 AlaLeuLeuLeuYsArgGlyValThrGluLeuAspGluLeuGluAlaAsnAspTrpAsnAsn 404  
Db 4842 GCGGGCAAGATCTATCGCGGATCGCGGGCGGAGTGGCGAAGCGGAATACGACACATC 4901  
QY 405 ThrArgAlaValSerLysProLysLysLeuLeuThrLeuPro----- 420  
Db 4902 ACCGGCGTGGCCACACAGCAAGCGCGCAAGCTGTGGCTGGTGGCGAATTCGCGATG 4961  
QY 421 IleAlaValAlaLysSerLeuValPro 429  
Db 4962 TCGCGGACGGCGACCTCGATGTCGCG 4988

## RESULT 13

US-09-939-964-1/c  
; Sequence 1, Application US/09939964  
; Publication No. US20030054522A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosenthal, Andre  
; APPLICANT: Freiberg, Christoph  
; APPLICANT: Perret, Xavier Philippe  
; APPLICANT: Broughton, William John  
; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic  
; FILE REFERENCE: CARP0068  
; CURRENT APPLICATION NUMBER: US/09/939,964  
; CURRENT FILING DATE: 2001-08-27  
; PRIOR APPLICATION NUMBER: 09/214,808  
; PRIOR FILING DATE: 1999-06-22  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 536165  
; TYPE: DNA  
; ORGANISM: Rhizobium  
US-09-939-964-1

## Alignment Scores:

Pred. No.:	1.58e-22	Length:	536165
Score:	233.00	Matches:	95
Percent Similarity:	46.75%	Conservative:	49
Best Local Similarity:	30.84%	Mismatches:	112
Query Match:	12.91%	Indels:	52
DB:	9	Gaps:	11



QY 273 ValGlyLeuMetSerValProValMetGlyIleAlaProGluSerLysAlaThrThrGlu 292  
 DB 1750 GTAGGTGAAGTATTGACGGCGATTTA-----AGTGATCATGAACACAT 1794  
 QY 293 SerValTyrAsnAlaLeuAlaLeuGlyLeuAlaAsnGlnLeuThrAsnIleLeuArg 312  
 DB 1795 CAGACATACGATGTCGCAAGAAGACTGTTGAATCGTTCAATTGATTATATTAAGA 1854  
 QY 313 AspValGlyGluAspAlaArgGlyArgValTyrLeuProGlnAspGluLeuAlaGln 332  
 DB 1855 GATGTCGGTGAAGATTTTGCACATGACGATGATATTTAGTAGCAACGATTAAGCAA 1914  
 QY 333 AlaGlyLeuSerAspGluAspIlePheAlaGlyArgValThrAspLysTyrArgAsnPhe 352  
 DB 1915 TATGAAGTTGATATTCCTGAAGTGACCAAAATGGTTTAATAATCATTTATGACTTA 1974  
 QY 353 MetLysGlyGlnIleGlnArgAlaArgLysPhePheAspGluSerGluLysGlyValThr 372  
 DB 1975 TGGGAATATATGACGCTATCGCAGAAAAAAGATTTTCAAGATGTTATGGATCAAAATC--- 2031  
 QY 373 GluLeuAspSerAlaSerArgTyrProValLeu---ThrAlaLeuLeuTyrArgLys 391  
 DB 2032 AAGTATTATGATTTGACGACACCAACCAATCATAGAAATTAGCAGACGATATATTTGAA 2091  
 QY 392 IleLeuAspGluIleGluAlaAsnAspTyrAsnAsnPheThrArgArgAlaTyrValSer 411  
 DB 2092 ATACTGACGAGTGTAGACGAGCTAACTAT---ACATTACATGACGCTGTTTGTGGAT 2148  
 QY 412 LysProLysLys 415  
 DB 2149 AAGAGGAAAAAG 2160

## RESULT 15

US-09-738-626-695  
 ; Sequence 695, Application US/09738626  
 ; Publication No. US20020197605A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NAKAGAWA, SATOSHI  
 ; APPLICANT: MIZOGUCHI, HIROSHI  
 ; APPLICANT: ANDO, SEIKO  
 ; APPLICANT: HAYASHI, MIKIO  
 ; APPLICANT: OCHIAI, KEIKO  
 ; APPLICANT: YOKOI, HARUHIKO  
 ; APPLICANT: TATEISHI, NAKO  
 ; APPLICANT: SENOH, AKIHIRO  
 ; APPLICANT: IKEDA, MASATO  
 ; APPLICANT: OZAKI, AKIO  
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
 ; FILE REFERENCE: 249-125  
 ; CURRENT APPLICATION NUMBER: US/09/738,626  
 ; CURRENT FILING DATE: 2000-12-18  
 ; PRIOR APPLICATION NUMBER: JP 99/377484  
 ; PRIOR FILING DATE: 1999-12-16  
 ; PRIOR APPLICATION NUMBER: JP 00/159162  
 ; PRIOR FILING DATE: 2000-04-07  
 ; PRIOR APPLICATION NUMBER: JP 00/280988  
 ; PRIOR FILING DATE: 2000-08-03  
 ; NUMBER OF SEQ ID NOS: 7059  
 ; SOFTWARE: Patent in ver. 3.0  
 ; SEQ ID NO 695  
 ; LENGTH: 912  
 ; TYPE: DNA  
 ; ORGANISM: Corynebacterium glutamicum  
 US-09-738-626-695

## Alignment Scores:

Pred. No.:	9,95e-16	Length:	912
Score:	204.00	Matches:	87
Percent Similarity:	41.45%	Conservative:	39
Best Local Similarity:	28.62%	Mismatches:	130
Query Match:	8.99%	Indels:	48
DB:	9	Gaps:	11

US-09-847-081b-2 (1-440) x US-09-738-626-695 (1-912)  
 QY 147 TyrAspArgCysGly-----GluValCysAlaGluTyrAlaLysThrPhe 161  
 DB 49 TACAATCGGCGCTCATTCAGGCTTCACATAAAGTCATGAAGAATATTCGACGAGCTTC 108  
 QY 162 TyrLeuGlyThrLysLeuMetThrProGluArgArgAlaIleThrPheAlaIleTyrVal 181  
 DB 109 ATCTGTCTACCTGGTGTCTATCCCGCCGATACGAAATGACATACGAAATCTCTATGCA 168  
 QY 182 TrpCysArgArgThrAspGluLeuValAspGlyProAsnAlaSerHisIleThrProGln 201  
 DB 169 GTAGTTCGTATCCCGATGAGATTGTCGAGCG-----ACTGCACAT 210  
 QY 202 AlaLeuAspArgTyrProGluThrArgLeuGluAspIlePheSerGlyArgProPheAspMet 221  
 DB 211 GCGCTGGTGTCTCAACTGCCAAAATCGAAGAGATTCTCGATGCCATGAAATTCGCGTT 270  
 QY 222 LeuAspAla-----AlaLeuSerAspThr 229  
 DB 271 CTGTCAGCCACCAACAACAGCTTCAACAGAGATCTTGTGTTTACAGCTTATGTTGAAC 330  
 QY 230 ValSerArgPheProValAspIleGlnProPheArgAspMetIleGluGlyMetArgMet 249  
 DB 331 GCCCGACGCTGTCATTTCCAAACAGAGCATGTAATAGCCTCTCTTCATCATCAATCGCTAG 390  
 QY 250 AspLeuTyrPheSerArgTyrLysThrPheAspGluLeuTyrLeuTyrCysTyrTyrVal 269  
 DB 391 GACCTC---AAAGCTAATACACAGCACCAGATAGTTCACACAGTATGCTATGGCTCC 447  
 QY 270 AlaGlyThrValGlyLeuMetSerValProValMetGlyIleAlaProGlu---SerLys 288  
 DB 448 GCGGAAGTTATAGGCTGCTTCTCTCAGCGTTTCAACCAAGTAGAAGATAGCAAA 507  
 QY 289 AlaThrThrGluSerValTyrAsnAlaAlaLeuAlaGlyLeuAlaAsnGlnLeuThr 308  
 DB 508 AACCGGTAGAGATTATGCAAAACGAGGCGCTCATTTGGGAGCGCATTCACAGAAAT 567  
 QY 309 AsnIleLeuArgAspValGlyGluAspAlaArgArg---GlyArgValTyrLeuProGln 327  
 DB 568 AACTTCTCCGTGACTTGGCAGAAGATCAGCAAAATTTGGGCGGATTTTATTTCCCGC--- 624  
 QY 328 AspGluLeuAlaGlnAlaGlyLeuSer-----AspGluAspIlePheAlaGlyArg 344  
 DB 625 ---AAAACCCCAAGGAATCTTCTACTAAGAACAAAAAGAGATCTCATCGCTGAT--- 678  
 QY 345 ValThrAspLysTyrArgAsnPheMetLysLysGlnIleGlnArgAlaArgLysPhePhe 364  
 DB 679 -----ATCCGTCAGACCTAGCAATTCGCCACGATGCATTT 714  
 QY 365 AspGluSerGluLysGlyValThrGluLeuAspSerAlaSerArgTyrProValLeuThr 384  
 DB 715 -----CCAGAAATACCAGTCGAGCTCGCATCGGAGTGATCTCT 753  
 QY 385 AlaLeuLeuTyrArgLysIleLeuAspGluIleGluAlaAsnAspTyrAsnAsnPhe 404  
 DB 754 GCTTATTTGCTCTTTCAAAAACCTACTACCGCAATTTAGGCTACTCTCTACCGCGCATTTA 813  
 QY 405 ThrArg---ArgAlaTyrValSerLysProLysLysLeuThrLeuProIleAlaTyr 423  
 DB 814 TTGCGGAGCGAATCAGAGTTCCACTTCATATCAAACTCTCTACACTCGGTAGAGCCACG 873  
 QY 424 AlaLysSerLeu 427  
 DB 874 ATGAAAAGGTCTA 885

Search completed: April 5, 2003, 05:21:58  
 Job time : 306 secs